

CL-2029USNA.ST25.txt  
SEQUENCE LISTING

<110> E. I. duPont de Nemours and Company, Inc.  
Cheng, Qiong  
Suh, Wonchul

<120> Mutations Affecting Plasmid Copy Number

<130> CL2029 US NA

<150> US 60/434973

<151> 2002-12-20

<160> 28

<170> PatentIn version 3.2

<210> 1

<211> 912

<212> DNA

<213> Pantoea stewartii

<220>

<221> misc\_feature

<222> (1)..(3)

<223> Alternative start code TTG instead of ATG used.

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ggtgccgcga tgcgtgaagg cacgctggca ccgggcaaac gtattcgtcc gatgctgctg	180
ttattaacag cgcgcgatct tggctgtgcg atcagtcacg ggggattact ggatttagcc	240
tgcgcggttg aaatggtgca tgctgcctcg ctgattctgg atgatatgcc ctgcatggac	300
gatgcgcaga tgcgtcgggg gcgtcccacc attcacacgc agtacggtga acatgtggcg	360
attctggcgg cggtcgcttt actcagcaaa gcgtttgggg tgattgccga ggctgaaggt	420
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gccatactgc taaccaatca gtttaaaacc agcacgctgt tttgcgcgtc aacgcaaattg	600
gcgtccattg cggccaacgc gtcctgcgaa gcgcgtgaga acctgcatcg tttctcgctc	660
gatctcggcc aggcctttca gttgcttgac gatcttaccg atggcatgac cgataccggc	720
aaagacatca atcaggatgc aggtaaatca acgctggtca atttattagg ctcaggcgcg	780
gtcgaagaac gcctgcgaca gcatttgcg ctggccagtg aacacctttc cgcggcgatgc	840
caaaacggcc attccaccac ccaacttttt attcaggcct ggtttgacaa aaaactcgct	900
gccgtcagtt aa	912

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<212> PRT

<213> Pantoea stewartii

<400> 2

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 20 25 30  
 Val Gln Gly Glu Arg Asp Cys Val Gly Ala Ala Met Arg Glu Gly Thr  
 35 40 45  
 Leu Ala Pro Gly Lys Arg Ile Arg Pro Met Leu Leu Leu Leu Thr Ala  
 50 55 60  
 Arg Asp Leu Gly Cys Ala Ile Ser His Gly Gly Leu Leu Asp Leu Ala  
 65 70 75 80  
 Cys Ala Val Glu Met Val His Ala Ala Ser Leu Ile Leu Asp Asp Met  
 85 90 95  
 Pro Cys Met Asp Asp Ala Gln Met Arg Arg Gly Arg Pro Thr Ile His  
 100 105 110  
 Thr Gln Tyr Gly Glu His Val Ala Ile Leu Ala Ala Val Ala Leu Leu  
 115 120 125  
 Ser Lys Ala Phe Gly Val Ile Ala Glu Ala Glu Gly Leu Thr Pro Ile  
 130 135 140  
 Ala Lys Thr Arg Ala Val Ser Glu Leu Ser Thr Ala Ile Gly Met Gln  
 145 150 155 160  
 Gly Leu Val Gln Gly Gln Phe Lys Asp Leu Ser Glu Gly Asp Lys Pro  
 165 170 175  
 Arg Ser Ala Asp Ala Ile Leu Leu Thr Asn Gln Phe Lys Thr Ser Thr  
 180 185 190  
 Leu Phe Cys Ala Ser Thr Gln Met Ala Ser Ile Ala Ala Asn Ala Ser  
 195 200 205  
 Cys Glu Ala Arg Glu Asn Leu His Arg Phe Ser Leu Asp Leu Gly Gln  
 210 215 220  
 Ala Phe Gln Leu Leu Asp Asp Leu Thr Asp Gly Met Thr Asp Thr Gly  
 225 230 235 240  
 Lys Asp Ile Asn Gln Asp Ala Gly Lys Ser Thr Leu Val Asn Leu Leu  
 245 250 255  
 Gly Ser Gly Ala Val Glu Glu Arg Leu Arg Gln His Leu Arg Leu Ala  
 260 265 270

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Ser Glu His Leu Ser Ala Ala Cys Gln Asn Gly His Ser Thr Thr Gln  
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 <222> (1)..(1296)

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 gct ctg caa aac ctt gct cag gaa tta gtg gcc cgc ggt cat cgt gtt 96  
 Ala Leu Gln Asn Leu Ala Gln Glu Leu Val Ala Arg Gly His Arg Val  
 20 25 30  
 acg ttt ttt cag caa cat gac tgc aaa gcg ctg gta acg ggc agc gat 144  
 Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp  
 35 40 45  
 atc gga ttc cag acc gtc gga ctg caa acg cat cct ccc ggt tcc tta 192  
 Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu  
 50 55 60  
 tcg cac ctg ctg cac ctg gcc gcg cac cca ctc gga ccc tcg atg tta 240  
 Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu  
 65 70 75 80  
 cga ctg atc aat gaa atg gca cgt acc agc gat atg ctt tgc cgg gaa 288  
 Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu  
 85 90 95  
 ctg ccc gcc gct ttt cat gcg ttg cag ata gag ggc gtg atc gtt gat 336  
 Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp  
 100 105 110  
 caa atg gag ccg gca ggt gca gta gtc gca gaa gcg tca ggt ctg ccg 384  
 Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro  
 115 120 125  
 ttt gtt tcg gtg gcc tgc gcg ctg ccg ctc aac cgc gaa ccg ggt ttg 432  
 Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu  
 130 135 140  
 cct ctg gcg gtg atg cct ttc gag tac ggc acc agc gat gcg gct cgg 480  
 Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg  
 145 150 155 160  
 gaa cgc tat acc acc agc gaa aaa att tat gac tgg ctg atg cga cgt 528  
 Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg  
 165 170 175  
 cac gat cgt gtg atc gcg cat cat gca tgc aga atg ggt tta gcc ccg 576  
 His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro  
 180 185 190

## CL-2029USNA.ST25.txt

cgt	gaa	aaa	ctg	cat	cat	tgt	ttt	tct	cca	ctg	gca	caa	atc	agc	cag	624
Arg	Glu	Lys	Leu	His	His	Cys	Phe	Ser	Pro	Leu	Ala	Gln	Ile	Ser	Gln	
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ttg	atc	ccc	gaa	ctg	gat	ttt	ccc	cgc	aaa	gcg	ctg	cca	gac	tgc	ttt	672
Leu	Ile	Pro	Glu	Leu	Asp	Phe	Pro	Arg	Lys	Ala	Leu	Pro	Asp	Cys	Phe	
	210					215					220					
cat	gcg	gtt	gga	ccg	tta	cgg	caa	ccc	cag	ggg	acg	ccg	ggg	tca	tca	720
His	Ala	Val	Gly	Pro	Leu	Arg	Gln	Pro	Gln	Gly	Thr	Pro	Gly	Ser	Ser	
					230					235					240	
act	tct	tat	ttt	ccg	tcc	ccg	gac	aaa	ccc	cgt	att	ttt	gcc	tcg	ctg	768
Thr	Ser	Tyr	Phe	Pro	Ser	Pro	Asp	Lys	Pro	Arg	Ile	Phe	Ala	Ser	Leu	
				245					250					255		
ggc	acc	ctg	cag	gga	cat	cgt	tat	ggc	ctg	ttc	agg	acc	atc	gcc	aaa	816
Gly	Thr	Leu	Gln	Gly	His	Arg	Tyr	Gly	Leu	Phe	Arg	Thr	Ile	Ala	Lys	
			260					265					270			
gcc	tgc	gaa	gag	gtg	gat	gcg	cag	tta	ctg	ttg	gca	cac	tgt	ggc	ggc	864
Ala	Cys	Glu	Glu	Val	Asp	Ala	Gln	Leu	Leu	Leu	Ala	His	Cys	Gly	Gly	
		275					280					285				
ctc	tca	gcc	acg	cag	gca	ggt	gaa	ctg	gcc	cgg	ggc	ggg	gac	att	cag	912
Leu	Ser	Ala	Thr	Gln	Ala	Gly	Glu	Leu	Ala	Arg	Gly	Gly	Asp	Ile	Gln	
	290					295					300					
gtt	gtg	gat	ttt	gcc	gat	caa	tcc	gca	gca	ctt	tca	cag	gca	cag	ttg	960
Val	Val	Asp	Phe	Ala	Asp	Gln	Ser	Ala	Ala	Leu	Ser	Gln	Ala	Gln	Leu	
	305				310					315					320	
aca	atc	aca	cat	ggt	ggg	atg	aat	acg	gta	ctg	gac	gct	att	gct	tcc	1008
Thr	Ile	Thr	His	Gly	Gly	Met	Asn	Thr	Val	Leu	Asp	Ala	Ile	Ala	Ser	
				325					330					335		
cgc	aca	ccg	cta	ctg	gcg	ctg	ccg	ctg	gca	ttt	gat	caa	cct	ggc	gtg	1056
Arg	Thr	Pro	Leu	Leu	Ala	Leu	Pro	Leu	Ala	Phe	Asp	Gln	Pro	Gly	Val	
			340					345					350			
gca	tca	cga	att	gtt	tat	cat	ggc	atc	ggc	aag	cgt	gcg	tct	cgg	ttt	1104
Ala	Ser	Arg	Ile	Val	Tyr	His	Gly	Ile	Gly	Lys	Arg	Ala	Ser	Arg	Phe	
		355					360					365				
act	acc	agc	cat	gcg	ctg	gcg	cgg	cag	att	cga	tcg	ctg	ctg	act	aac	1152
Thr	Thr	Ser	His	Ala	Leu	Ala	Arg	Gln	Ile	Arg	Ser	Leu	Leu	Thr	Asn	
		370				375					380					
acc	gat	tac	ccg	cag	cgt	atg	aca	aaa	att	cag	gcc	gca	ttg	cgt	ctg	1200
Thr	Asp	Tyr	Pro	Gln	Arg	Met	Thr	Lys	Ile	Gln	Ala	Ala	Leu	Arg	Leu	
					390					395					400	
gca	ggc	ggc	aca	cca	gcc	gcc	gcc	gat	att	gtt	gaa	cag	gcg	atg	cgg	1248
Ala	Gly	Gly	Thr	Pro	Ala	Ala	Ala	Asp	Ile	Val	Glu	Gln	Ala	Met	Arg	
				405					410					415		
acc	tgt	cag	cca	gta	ctc	agt	ggg	cag	gat	tat	gca	acc	gca	cta	tga	1296
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 Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp  
 35 40 45  
 Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu  
 50 55 60  
 Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu  
 65 70 75 80  
 Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu  
 85 90 95  
 Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp  
 100 105 110  
 Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro  
 115 120 125  
 Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu  
 130 135 140  
 Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg  
 145 150 155 160  
 Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg  
 165 170 175  
 His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro  
 180 185 190  
 Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln  
 195 200 205  
 Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe  
 210 215 220  
 His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser  
 225 230 235 240  
 Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu  
 245 250 255  
 Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys  
 260 265 270

Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly  
 275 280 285

Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln  
 290 295 300

Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu  
 305 310 315 320

Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser  
 325 330 335

Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val  
 340 345 350

Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe  
 355 360 365

Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn  
 370 375 380

Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu  
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<220>  
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ggc ctt atc gcg ctc cgg ctt cag caa cag cat ccg gat atg cgg atc 96  
 Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln His Pro Asp Met Arg Ile  
 20 25 30

ttg ctt att gag gcg ggt cct gag gcg gga ggg aac cat acc tgg tcc 144  
 Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser  
 35 40 45

ttt cac gaa gag gat tta acg ctg aat cag cat cgc tgg ata gcg ccg 192  
 Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro  
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ctt gtg gtc cat cac tgg ccc gac tac cag gtt cgt ttc ccc caa cgc 240

Leu 65	Val	Val	His	His	Trp 70	Pro	Asp	Tyr	Gln	Val 75	Arg	Phe	Pro	Gln	Arg 80	
cgt Arg	cgc Arg	cat His	gtg Val	aac Asn 85	agt Ser	ggc Gly	tac Tyr	tac Tyr	tgc Cys 90	gtg Val	acc Thr	tcc Ser	cgg Arg	cat His 95	ttc Phe	288
gcc Ala	ggg Gly	ata Ile	ctc Leu 100	cgg Arg	caa Gln	cag Gln	ttt Phe	gga Gly 105	caa Gln	cat His	tta Leu	tgg Trp	ctg Leu 110	cat His	acc Thr	336
gcg Ala	gtt Val	tca Ser 115	gcc Ala	gtt Val	cat His	gct Ala	gaa Glu 120	tcg Ser	gtc Val	cag Gln	tta Leu	gcg Ala 125	gat Asp	ggc Gly	cgg Arg	384
att Ile	att Ile 130	cat His	gcc Ala	agt Ser	aca Thr	gtg Val 135	atc Ile	gac Asp	gga Gly	cgg Arg	ggt Gly 140	tac Tyr	acg Thr	cct Pro	gat Asp	432
tct Ser 145	gca Ala	cta Leu	cgc Arg	gta Val	gga Gly 150	ttc Phe	cag Gln	gca Ala	ttt Phe	atc Ile 155	ggt Gly	cag Gln	gag Glu	tgg Trp	caa Gln 160	480
ctg Leu	agc Ser	gcg Ala	ccg Pro	cat His 165	ggt Gly	tta Leu	tcg Ser	tca Ser	ccg Pro 170	att Ile	atc Ile	atg Met	gat Asp	gcg Ala 175	acg Thr	528
gtc Val	gat Asp	cag Gln	caa Gln 180	aat Asn	ggc Gly	tac Tyr	cgc Arg	ttt Phe 185	gtt Val	tat Tyr	acc Thr	ctg Leu	ccg Pro 190	ctt Leu	tcc Ser	576
gca Ala	acc Thr	gca Ala 195	ctg Leu	ctg Leu	atc Ile	gaa Glu	gac Asp 200	aca Thr	cac His	tac Tyr	att Ile	gac Asp 205	aag Lys	gct Ala	aat Asn	624
ctt Leu	cag Gln 210	gcc Ala	gaa Glu	cgg Arg	gcg Ala	cgt Arg 215	cag Gln	aac Asn	att Ile	cgc Arg	gat Asp 220	tat Tyr	gct Ala	gcg Ala	cga Arg	672
cag Gln 225	ggt Gly	tgg Trp	ccg Pro	tta Leu	cag Gln 230	acg Thr	ttg Leu	ctg Leu	cgg Arg	gaa Glu 235	gaa Glu	cag Gln	ggt Gly	gca Ala	ttg Leu 240	720
ccc Pro	att Ile	acg Thr	tta Leu	acg Thr 245	ggc Gly	gat Asp	aat Asn	cgt Arg	cag Gln 250	ttt Phe	tgg Trp	caa Gln	cag Gln	caa Gln 255	ccg Pro	768
caa Gln	gcc Ala	tgt Cys	agc Ser 260	gga Gly	tta Leu	cgc Arg	gcc Ala	ggg Gly 265	ctg Leu	ttt Phe	cat His	ccg Pro	aca Thr 270	acc Thr	ggc Gly	816
tac Tyr	tcc Ser	cta Leu 275	ccg Pro	ctc Leu	gcg Ala	gtg Val	gcg Ala 280	ctg Leu	gcc Ala	gat Asp	cgt Arg	ctc Leu 285	agc Ser	gcg Ala	ctg Leu	864
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cag Gln 305	caa Gln	cgt Arg	tgg Trp	cag Gln	caa Gln 310	cag Gln	ggg Gly	ttt Phe	ttc Phe	cgc Arg 315	atg Met	ctg Leu	aat Asn	cgc Arg	atg Met 320	960
ttg Leu	ttt Phe	tta Leu	gcc Ala	gga Gly 325	ccg Pro	gcc Ala	gag Glu	tca Ser	cgc Arg 330	tgg Trp	cgt Arg	gtg Val	atg Met	cag Gln 335	cgt Arg	1008
ttc	tat	ggc	tta	ccc	gag	gat	ttg	att	gcc	cgc	ttt	tat	gcg	gga	aaa	1056

Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys  
 340 345 350

ctc acc gtg acc gat cgg cta cgc att ctg agc ggc aag ccg ccc gtt 1104  
 Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val  
 355 360 365

ccc gtt ttc gcg gca ttg cag gca att atg acg act cat cgt tga 1149  
 Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg  
 370 375 380

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 <213> Pantoea stewartii

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Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser  
 35 40 45

Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro  
 50 55 60

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg  
 65 70 75 80

Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe  
 85 90 95

Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr  
 100 105 110

Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg  
 115 120 125

Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp  
 130 135 140

Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln  
 145 150 155 160

Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr  
 165 170 175

Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser  
 180 185 190

Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn  
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Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg  
210 215 220  
Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu  
225 230 235 240  
Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Gln Pro  
245 250 255  
Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly  
260 265 270  
Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu  
275 280 285  
Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala  
290 295 300  
Gln Gln Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met  
305 310 315 320  
Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg  
325 330 335  
Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys  
340 345 350  
Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val  
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Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg  
370 375 380

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<220>  
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gca att cgt tta cag gcc gca ggt att cct gtt ttg ctg ctt gag cag 96  
Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln  
20 25 30  
cgc gac aag ccg ggt ggc cgg gct tat gtt tat cag gag cag ggc ttt 144  
Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe

35	40	45	
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gga Glu 65	ctg Leu 70	ttt Phe 75	gct Ala 80
ttg Leu 85	ccg Pro 90	gtc Val 95	acg Thr 100
ttc Phe 105	aat Asn 110	tac Tyr 115	gat Asp 120
ttt Phe 125	aat Asn 130	ccg Pro 135	cg Arg 140
cgt Arg 145	gcc Ala 150	gta Val 155	ttc Phe 160
tta Leu 165	tcg Ser 170	ttc Phe 175	aaa Lys 180
cag Gln 185	gca Ala 190	tgg Trp 195	cg Arg 200
gag Glu 205	cat His 210	ctt Leu 215	cg Arg 220
aat Asn 225	ccg Pro 230	ttt Phe 235	gca Ala 240
aat Asn 245	gcc Ala 250	cg Arg 255	gtc Val 260
gtg Val 265	cag Gln 270	ttg Leu 275	gaa Glu 280
aac Asn 285	gct Ala 290	gat Asp 295	gtt Val 300
gca Ala 305	gcc Ala 310	gct Ala 315	aag Lys 320
tca Ser 325	ctg Leu 330	ttt Phe 335	gta Val 340
ctc Leu 345	tat Tyr 350	ttt Phe 355	ggt Gly 360
ctc Leu 365	aac Asn 370	cat His 375	cat His 380
cat His 385	cac His 390	gat Asp 395	caa Gln 400
ctc Leu 405	ctc Leu 410	ctc Leu 415	ctc Leu 420

## CL-2029USNA.ST25.txt

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Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His							
		325		330		335	
gaa att ttt aac cat gat ggt ctg gct gag gat ttt tcg ctt tat tta							1056
Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu							
		340		345		350	
cac gca cct tgt gtc acg gat ccg tca ctg gca ccg gaa ggg tgc ggc							1104
His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly							
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agc tat tat gtg ctg gcg cct gtt cca cac tta ggc acg gcg aac ctc							1152
Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu							
		370		375		380	
gac tgg gcg gta gaa gga ccc cga ctg cgc gat cgt att ttt gac tac							1200
Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr							
		385		390		395	400
ctt gag caa cat tac atg cct ggc ttg cga agc cag ttg gtg acg cac							1248
Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His							
		405		410		415	
cgt atg ttt acg ccg ttc gat ttc cgc gac gag ctc aat gcc tgg caa							1296
Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln							
		420		425		430	
ggt tcg gcc ttc tcg gtt gaa cct att ctg acc cag agc gcc tgg ttc							1344
Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe							
		435		440		445	
cga cca cat aac cgc gat aag cac att gat aat ctt tat ctg gtt ggc							1392
Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly							
		450		455		460	
gca ggc acc cat cct ggc gcg ggc att ccc ggc gta atc ggc tcg gcg							1440
Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala							
		465		470		475	480
aag gcg acg gca ggc tta atg ctg gag gac ctg att tga							1479
Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile							
		485		490			

<210> 8  
 <211> 492  
 <212> PRT  
 <213> Pantoea stewartii

<400> 8

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Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe  
35 40 45

Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu  
50 55 60

Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Asp Tyr Val Glu Leu  
 65 70 75 80  
 Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val  
 85 90 95  
 Phe Asn Tyr Asp Asn Asp Gln Ala Gln Leu Glu Ala Gln Ile Gln Gln  
 100 105 110  
 Phe Asn Pro Arg Asp Val Ala Gly Tyr Arg Ala Phe Leu Asp Tyr Ser  
 115 120 125  
 Arg Ala Val Phe Asn Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe  
 130 135 140  
 Leu Ser Phe Lys Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu  
 145 150 155 160  
 Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Gly Tyr Ile Glu Asp  
 165 170 175  
 Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly  
 180 185 190  
 Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu  
 195 200 205  
 Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val  
 210 215 220  
 Asn Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu  
 225 230 235 240  
 Asn Ala Arg Val Ser His Met Glu Thr Val Gly Asp Lys Ile Gln Ala  
 245 250 255  
 Val Gln Leu Glu Asp Gly Arg Arg Phe Glu Thr Cys Ala Val Ala Ser  
 260 265 270  
 Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro  
 275 280 285  
 Ala Ala Ala Lys Gln Ala Lys Lys Leu Gln Ser Lys Arg Met Ser Asn  
 290 295 300  
 Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu  
 305 310 315 320  
 Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His  
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Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu  
 340 345 350  
 His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly  
 355 360 365  
 Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu  
 370 375 380  
 Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr  
 385 390 395 400  
 Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His  
 405 410 415  
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln  
 420 425 430  
 Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe  
 435 440 445  
 Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly  
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 Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala  
 465 470 475 480  
 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile  
 485 490

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 <212> DNA  
 <213> *Pantoea stewartii*

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 <222> (1)..(891)

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 gcc aaa acc cgt cgc agc gtg ctg atg ctt tac gca tgg tgc cgc cac 96  
 Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His  
 20 25 30  
 tgc gac gac gtc att gac gat caa aca ctg ggc ttt cat gcc gac cag 144  
 Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln  
 35 40 45  
 ccc tct tcg cag atg cct gag cag cgc ctg cag cag ctt gaa atg aaa 192  
 Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Leu Glu Met Lys  
 50 55 60

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gcg	ttt	cag	gag	gtc	gcg	atg	gcg	cat	gat	atc	gct	ccc	gcc	tac	gcg	288
Ala	Phe	Gln	Glu	Val	Ala	Met	Ala	His	Asp	Ile	Ala	Pro	Ala	Tyr	Ala	
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ttc	gac	cat	ctg	gaa	ggt	ttt	gcc	atg	gat	gtg	cgc	gaa	acg	cgc	tac	336
Phe	Asp	His	Leu	Glu	Gly	Phe	Ala	Met	Asp	Val	Arg	Glu	Thr	Arg	Tyr	
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ctg	aca	ctg	gac	gat	acg	ctg	cgt	tat	tgc	tat	cac	gtc	gcc	ggt	gtt	384
Leu	Thr	Leu	Asp	Asp	Thr	Leu	Arg	Tyr	Cys	Tyr	His	Val	Ala	Gly	Val	
		115					120					125				
gtg	ggc	ctg	atg	atg	gcg	caa	att	atg	ggc	gtt	cgc	gat	aac	gcc	acg	432
Val	Gly	Leu	Met	Met	Ala	Gln	Ile	Met	Gly	Val	Arg	Asp	Asn	Ala	Thr	
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ctc	gat	cgc	gcc	tgc	gat	ctc	ggg	ctg	gct	ttc	cag	ttg	acc	aac	att	480
Leu	Asp	Arg	Ala	Cys	Asp	Leu	Gly	Leu	Ala	Phe	Gln	Leu	Thr	Asn	Ile	
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gcg	cgt	gat	att	gtc	gac	gat	gct	cag	gtg	ggc	cgc	tgt	tat	ctg	cct	528
Ala	Arg	Asp	Ile	Val	Asp	Asp	Ala	Gln	Val	Gly	Arg	Cys	Tyr	Leu	Pro	
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gaa	agc	tgg	ctg	gaa	gag	gaa	gga	ctg	acg	aaa	gcg	aat	tat	gct	gcg	576
Glu	Ser	Trp	Leu	Glu	Glu	Glu	Gly	Leu	Thr	Lys	Ala	Asn	Tyr	Ala	Ala	
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cca	gaa	aac	cgg	cag	gcc	tta	agc	cgt	atc	gcc	ggg	cga	ctg	gta	cgg	624
Pro	Glu	Asn	Arg	Gln	Ala	Leu	Ser	Arg	Ile	Ala	Gly	Arg	Leu	Val	Arg	
		195					200					205				
gaa	gcg	gaa	ccc	tat	tac	gta	tca	tca	atg	gcc	ggt	ctg	gca	caa	tta	672
Glu	Ala	Glu	Pro	Tyr	Tyr	Val	Ser	Ser	Met	Ala	Gly	Leu	Ala	Gln	Leu	
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ccc	tta	cgc	tcg	gcc	tgg	gcc	atc	gcg	aca	gcg	aag	cag	gtg	tac	cgt	720
Pro	Leu	Arg	Ser	Ala	Trp	Ala	Ile	Ala	Thr	Ala	Lys	Gln	Val	Tyr	Arg	
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aaa	att	ggc	gtg	aaa	gtt	gaa	cag	gcc	ggt	aag	cag	gcc	tgg	gat	cat	768
Lys	Ile	Gly	Val	Lys	Val	Glu	Gln	Ala	Gly	Lys	Gln	Ala	Trp	Asp	His	
				245					250					255		
cgc	cag	tcc	acg	tcc	acc	gcc	gaa	aaa	tta	acg	ctt	ttg	ctg	acg	gca	816
Arg	Gln	Ser	Thr	Ser	Thr	Ala	Glu	Lys	Leu	Thr	Leu	Leu	Leu	Thr	Ala	
			260					265					270			
tcc	ggt	cag	gca	gtt	act	tcc	cgg	atg	aag	acg	tat	cca	ccc	cgt	cct	864
Ser	Gly	Gln	Ala	Val	Thr	Ser	Arg	Met	Lys	Thr	Tyr	Pro	Pro	Arg	Pro	
		275					280					285				
gct	cat	ctc	tgg	cag	cgc	ccg	atc	tag								891
Ala	His	Leu	Trp	Gln	Arg	Pro	Ile									
	290					295										

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 <211> 296  
 <212> PRT  
 <213> Pantoea stewartii  
 <400> 10

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 Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His  
 20 25 30  
 Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln  
 35 40 45  
 Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys  
 50 55 60  
 Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala  
 65 70 75 80  
 Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala  
 85 90 95  
 Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr  
 100 105 110  
 Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val  
 115 120 125  
 Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr  
 130 135 140  
 Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile  
 145 150 155 160  
 Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro  
 165 170 175  
 Glu Ser Trp Leu Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala  
 180 185 190  
 Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg  
 195 200 205  
 Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu  
 210 215 220  
 Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg  
 225 230 235 240  
 Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His  
 245 250 255  
 Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala  
 260 265 270

Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro  
 275 280 285

Ala His Leu Trp Gln Arg Pro Ile  
 290 295

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 <212> DNA  
 <213> Pantoea stewartii

<220>  
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 <222> (1)..(528)

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 atg gaa gtg gtt gct gca ctg gca cat aaa tac atc atg cac ggc tgg 96  
 Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp  
 20 25 30  
 ggt tgg ggc tgg cat ctt tca cat cat gaa ccg cgt aaa ggc gca ttt 144  
 Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe  
 35 40 45  
 gaa gtt aac gat ctc tat gcc gtg gta ttc gcc att gtg tcg att gcc 192  
 Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala  
 50 55 60  
 ctg att tac ttc ggc agt aca gga atc tgg ccg ctc cag tgg att ggt 240  
 Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly  
 65 70 75 80  
 gca ggc atg acc gct tat ggt tta ctg tat ttt atg gtc cac gac gga 288  
 Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly  
 85 90 95  
 ctg gta cac cag cgc tgg ccg ttc cgc tac ata ccg cgc aaa ggc tac 336  
 Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr  
 100 105 110  
 ctg aaa cgg tta tac atg gcc cac cgt atg cat cat gct gta agg gga 384  
 Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly  
 115 120 125  
 aaa gag ggc tgc gtg tcc ttt ggt ttt ctg tac gcg cca ccg tta tct 432  
 Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser  
 130 135 140  
 aaa ctt cag gcg acg ctg aga gaa agg cat gcg gct aga tcg ggc gct 480  
 Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala  
 145 150 155 160  
 gcc aga gat gag cag gac ggg gtg gat acg tct tca tcc ggg aag taa 528  
 Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys  
 165 170 175

<210> 12  
 <211> 175  
 <212> PRT



&lt;213&gt; Pantoea stewartii

&lt;400&gt; 12

Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly  
 1 5 10 15

Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp  
 20 25 30

Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe  
 35 40 45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala  
 50 55 60

Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly  
 65 70 75 80

Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly  
 85 90 95

Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr  
 100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly  
 115 120 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser  
 130 135 140

Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala  
 145 150 155 160

Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys  
 165 170 175

&lt;210&gt; 13

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer used to amplify crt gene cluster.

&lt;400&gt; 13

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25

&lt;210&gt; 14

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer used to amplify crt gene cluster.

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<210> 15  
 <211> 21  
 <212> DNA  
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<220>  
 <223> Primer Tn5PCRF

<400> 15  
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<210> 16  
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<220>  
 <223> Primer Tn5PCRR

<400> 16  
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 <212> DNA  
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<400> 17  
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<210> 18  
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 <212> DNA  
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 <223> Primer Kan-2 RP-1

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<210> 19  
 <211> 3159  
 <212> DNA  
 <213> Escherichia coli

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 aatggcgaac tggttgatgc ttgcgatctg attgaaaacg acgcacaact gtcgatcatt 180  
 accgccaaag acgaagaagg tctggagatc attcgtcact cctgtgcgca cctgttaggg 240  
 cacgcgatta aacaactttg gccgcatacc aaaatggcaa tcggcccgggt tattgacaac 300

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 <213> Escherichia coli

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